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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/347,064A

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This Raw Listing contains the General Information
Section and up to first 5 pages.

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1  <110> APPLICANT: Eck, Jurgen
2      Schmidt, Arno
3      Zinke, Holger
4  <120> TITLE OF INVENTION: Recombinant Fusion Proteins Based on
5      Ribosome-Inactivating Proteins of the mistletoe Viscum
6      album
7  <130> FILE REFERENCE: 09282-5
8  <140> CURRENT APPLICATION NUMBER: US/09/347,064A
9  <141> CURRENT FILING DATE: 1999-07-02
10 <150> EARLIER APPLICATION NUMBER: PCT/EP98/00009
11 <151> EARLIER FILING DATE: 1998-01-02
12 <150> EARLIER APPLICATION NUMBER: EP 97 10 0012.0
13 <151> EARLIER FILING DATE: 1997-01-02
14 <160> NUMBER OF SEQ ID NOS: 38
15 <170> SOFTWARE: PatentIn Ver. 2.1
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17 <211> LENGTH: 762
18 <212> TYPE: DNA
19 <213> ORGANISM: Viscum album
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23      ctcttgctgc agtctacgat ccccgctctcc gatgcgcgaaa gatttgtctt ggtggagctc 180
24      accaaccagg ggggagactc gatcacggcc gccatcgacg ttaccaatct gtacgtcgtg 240
25      gcttaccagc caggcgacca atcctacttt ttgcgcgacg caccacgcgg cgcggaacg 300
26      catctcttca ccggcaccac ccgatcctct ctcccattca acggaagcta cctgatctg 360
27      gagcgatacg ccggacatag ggaccagatc cctctcggtg tagaccaact cattcaatcc 420
28      gtcacggcgc ttcgttttcc gggcggcgac acgcgtaccc aagctcggtc gattttaatc 480
29      ctcattcaga tgatctccga ggccgccaga ttcaatccca tcttatggag ggctcgccaa 540
30      tacattaaca gtggggcgctc atttctgcca gacgtgtaca tgctggagct ggagacgagt 600
31      tggggccaac aatccacgca agtccagcat tcaaccgatg gcgtttttaa taaccaatt 660
32      cggttggcta taccctcccg taacttcgtg acgttgacca atgttcgcga cgtgatcgcc 720
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35 <211> LENGTH: 252
36 <212> TYPE: PRT
37 <213> ORGANISM: Viscum album
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40      1          5          10          15
41      Glu Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly
42      20          25          30
43      Ser Phe Ser Asn Glu Ile Pro Leu Arg Gln Ser Thr Ile Pro Val
44      35          40          45

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47      Asp Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala
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49      Tyr Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly
50          85          90          95
51      Ala Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe
52          100         105         110
53      Asn Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln
54          115         120         125
55      Ile Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg
56          130         135         140
57      Phe Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu
58          145         150         155         160
59      Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg
60          165         170         175
61      Ala Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr
62          180         185         190
63      Met Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln
64          195         200         205
65      His Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro
66          210         215         220
67      Pro Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser
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82      ggcactacgc ttacggtgca aacactggat tacacgttgg gacagggctg gcttgccggt 420
83      aatgataccg cccacgcgca ggtgaccata tatgggttca gggaccttgg catggaatca 480
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86      agagactccg tttcaacagt aatcaatata gttagctgca gcgctggatc gtctgggcag 660
87      cgatgggtgt ttaccaatga aggggccatt ttgaatttaa agaatgggtt ggccatggat 720
88      gtggcgcaag caaatccaaa gtcgcgccga ataactatct atcctgccac aggaaaaacca 780
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91      <211> LENGTH: 267
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95      Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly
96      1          5          10          15
97      Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Phe Arg Asp Gly
98      20          25          30
99      Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
100     35          40          45
101     Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
102     50          55          60
103     Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
104     65          70          75          80
105     Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn
106     85          90          95
107     Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
108     100         105         110
109     Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
110     115         120         125
111     Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
112     130         135         140
113     Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
114     145         150         155         160
115     Trp Val Glu Thr Cys Val Ser Ser Gln Lys Asn Gln Arg Trp Ala Leu
116     165         170         175
117     Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu
118     180         185         190
119     Thr Cys Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys
120     195         200         205
121     Ser Ala Gly Ser Ser Gly Gln Arg Trp Val Phe Thr Asn Glu Gly Ala
122     210         215         220
123     Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala Asn
124     225         230         235         240
125     Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro Asn
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131 <212> TYPE: DNA

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136 <211> LENGTH: 16

137 <212> TYPE: PRT

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141 1 5 10 15

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143 <211> LENGTH: 756

144 <212> TYPE: DNA

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149     cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttggtgga gctcaccaac 180
150     caggggggag actcgatcac ggcgcgcac gacgttacca atctgtacgt cgtggcctac 240
151     caagcaggcg accaatccta ctttttgcgc gacgcaccac gcggcgcgga aacgcatttc 300
152     ttcaccggca ccacccgatc ctctctccca ttcaacggaa gctaccctga tctggagcga 360
153     tacgccggac atagggacca gatccctctc ggtatagacc aactcattca atccgtcacg 420
154     gcgcttcggt ttccgggcgg cagcacgcgt acccaagctc gttcgatttt aatcctcatt 480
155     cagatgatct ccgaggccgc cagattcaat cccatcttat ggagggctcg ccaatacatt 540
156     aacagtgggg cgtcatttct gccagacgtg tacatgctgg agctggagac gagttggggc 600
157     caacaatcca cgcaagtcca gcattcaacc gatggcggtt ttaataaccc aattcggttg 660
158     gctatacccc ccggtaaatt cgtgacgttg accaatgttc gcgacgtgat cgccagcttg 720
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168             20             25             30
169     Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser
170             35             40             45
171     Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly Asp
172             50             55             60
173     Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala Tyr
174             65             70             75             80
175     Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly Ala
176             85             90             95
177     Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn
178             100            105            110
179     Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile
180             115            120            125
181     Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe
182             130            135            140
183     Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile
184             145            150            155            160
185     Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala
186             165            170            175
187     Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met
188             180            185            190
189     Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln His
190             195            200            205
191     Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro
192             210            215            220
193     Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu
194             225            230            235            240

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204      aagtccaaca atgatccgaa tcagttgttg acgatcaaaa gggatggaac cattcgatcc 180
205      aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
206      tgtaatactg ctgtgcggga ggccactctt tggcagatat ggggcaatgg gaccatcatc 300
207      aatccaagat ccaatctggt tttggcagca tcatctggaa tcaaaggcac tacgcttacg 360
208      gtgcaaacac tggattacac gttgggacag ggctggcttg ccggtaatga taccgccccca 420
209      cgcgagggtga ccatatatgg gttcagggac ctttgcattg aatcaaattg agggagtgtg 480
210      tgggtggaga cgtgcgtgag tagccaaaag aaccaaagat gggctttgta cggggatggg 540
211      tctatacgcc ccaaacaaaa ccaagaccaa tgcctcacct gtgggagaga ctccgtttca 600
212      acagtaatca atatatgttag ctgcagcgct ggatcgtctg ggacgcgatg ggtgtttacc 660
213      aatgaagggg ccattttgaa tttaaagaat gggttggcca tggatgtggc gcaagcaaat 720
214      ccaaagctcc gccgaataat catctatcct gccacaggaa aaccaaatac aatgtggctt 780
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223      Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Asp Phe Arg Asp Gly
224      20          25          30
225      Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
226      35          40          45
227      Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
228      50          55          60
229      Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
230      65          70          75          80
231      Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn
232      85          90          95
233      Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
234      100         105         110
235      Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
236      115         120         125
237      Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
238      130         135         140
239      Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
240      145         150         155         160
241      Trp Val Glu Thr Cys Val Ser Ser Gln Lys Asn Gln Arg Trp Ala Leu
242      165         170         175
243      Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu
244      180         185         190

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